

Sequence of BCLGA (Green) clones from BaF3 library

GAATTCGGCAGAGCTCCCTCCTCCCTCCTTCCTTCCTTCCTCCCTTCTCCCTC  
1 -----+-----+-----+-----+-----+-----+-----+ 60  
CTTAAGCCGTGCTCGAGGGGAGGAGGGAGGAAGGAAGGAAGGAGGGAAAGAGGGAG

61 CCTCCCTCCCTCCCTCCCAGTCTCCACCAGGAAACAACCGGATTCGGATCCCGGCTGC  
-----+-----+-----+-----+-----+-----+ 120  
CGAGGGCAGGGAGGGAGGGTCAGGAGGTGGTCTTTGTTGGCCTAAGGCCTAGGGCCGACG

GGCCTGACCCGGCTCCACTCTAGCCGGGAGGATGAAAGGCCTCAGCTGGGGGCTCCCTGC

121 -----+-----+-----+-----+ 180  
CCGGACTGGGCCGAGGTGAGATCGGCCCTCCTACTTTCCGGAGTCGACCCCGAGGGACG

CACCAGCACTGGGTCCCTAAGAGCTGCCATCCAGGCTGGCCGCCCGGATGGCGACCCAGC  
181 -----+-----+-----+-----+ 240  
GTGGTCGTGACCCAGGATTCTCGACGGTAGGTCCGACCGGGGGCCTACCGCTGGGGTCG

CTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTATAAGCTGAGGCAGAA  
241 -----+-----+-----+-----+ 300  
GAGTGGGGTCTGTGTGCCCCGAGATCACCGACTGAAACATCCGATATTCGACTCCGTCTT

GGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGACCCGCTGCACCAAGC  
301 -----+-----+-----+-----+ 360

CCCAATACAGACACCTCGACCGGGACCCCTTCCGGGTCGGCGGCTGGGCGACGTGGTTCG

361 CATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTCCGCCGCACCTTCTCTGACCTGGC 420  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
GTACGCGCGACGACCTCTGCTCAAACCTCTGGGCAAAGGCGGCGTGGAAGAGACTGGACCG

421 CGCTCAGCTACACGTGACCCCAAGGCTCAGCCCAGCAACGCTTCACCCAGGTTCCGACGA 480  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
GCGACTCGATGTGCACTGGGGTCCGAGTCGGGTCGTTGCGAACTGGGTCCAAAGGCTGCT

481 ACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCCTTGTCGATTCTTTGTCTTTGGGGCTGC 540  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
TGAAAAGGTTCCCCCGGATTGACCCCGGCAGAACCCGTAAGAAACAGAAACCCCGACG

541 CCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGACAAGTGCAGGATTG 600  
-----+-----+  
GGACACACGACTCTCACAGTTGTTTCTTTACCTCGGAAACCACCCTGTTACGTCCTAAC

601 GATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGCAGTGGGGGCTGGGC 660  
-----+-----+  
CTACCACCGGATGGACCTCTGTGCAGACCGACTGACCTAGGTGTCGTCACCCCCGACCCG

661 GGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGG 720  
-----+-----+  
CCTCAAGTGTCGAGATATGCCCCGCCCCGGGACCTCCTCCGTGCCGCAGACGCCCTCCC

GAAGTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGGTAAC  
721 -----+-----+-----+-----+-----+-----+-----+ 780  
CTTGACCCGTAGTCACTCCTGTCACGACTGCCCCCGGCACCGTGACCCCGGGACCATTG

.....  
TGTAGGGGCCTTTTTGCTAGCAAGTGAGAAAGTCTAGGGCCAGGTGGGGCTAGGTGTGG  
781 -----+-----+-----+-----+-----+-----+-----+ 840  
ACATCCCGGAAAAACGATCGTTCACCTCTTTCAGATCCCGGTCCACCCCGATCCACACC

CTAGGGGCCAGGAGAGCTGGAACAATAGCGAATGCCCTTGGGAAGAACTGGATGTCACGG  
841 -----+-----+-----+-----+-----+-----+-----+ 900  
GATCCCGGTCTCTCGACCTTGTTATCGCTTACGGGAACCTTCTTTGACCTACAGTGCC

AACAGAGAAAGGCAGGGGAAGGTAGTGTGTGTGGGAGCCCATCATCCAGGCAGGTGGCA  
901 -----+-----+-----+-----+ 960  
TTGTCTCTTTCCGTCCCCTTCCATCACACACACCCTCGGGTAGTAGGGTCCGTCCACCGT

GGGAGAATGAGTTGGAAACATTAAGGAATGTTCAAGGCCTAGAACCCAGAGAGTGGAGT  
961 -----+-----+-----+-----+ 1020  
CCCTCTTACTCAACCTTTGTAATTCCTTACAAAGTTCCGGATCTTGGGTCTCTCACCTCA

CATCCACGGCTTGGGGGGTGGGGGTGGGGAGGTGGGATGAATCATGCCCATATCGCGGG  
1021 -----+-----+-----+-----+ 1080  
GTAGGGTGCCGAACCCCCACCCCCACCCCTCCACCCTACTTAGTACGGGTATAGCGCCC

CACACAACCTACCCGGAACATGGCTTGTAGCTCCCAAGGACGGTGAGCTTACTTCANAGAT  
1081 -----+-----+-----+-----+-----+ 1140  
GTGTGTTGATGGGCCTTGTACCGAACATCGAGGGTTCCTGCCACTCGAATGAAGTNTCTA

CTGTGTCTCGACTAGATGAATGGGATTTAGGAGCCTAGAATTCACTTCCCTTTGGGATGG  
1141 -----+-----+-----+-----+-----+ 1200  
GACACAGAGCTGATCTACTTACCCTAAATCCTCGGATCTTAAGTGAAGGGAACCCCTACC

AAGCTTGGTGATCAGGTGACTGGGTGAAATGGCTGTGGCTGTGGGCTGCATGGGCACACC  
1201 -----+-----+-----+-----+-----+ 1260  
TTCGAACCACTAGTCCACTGACCCACTTTACCGACACCGACACCCGACGTACCCGTGTGG

TGTGCATGTATGTGCACATGCAAGCATGCTCATGTGCATGCTGGGCTGTCTGTCTGAATCT  
1261 -----+-----+-----+-----+-----+ 1320  
ACACGTACATACACGTGTACGTTTCGTACGAGTACACGTACGACCCGACAGACAGCTTAGA

GGTGGTGGGGTACTTAGAGAAAACATTCCTTCTTGCTATGGCAAGAACAAGGGGCAGTTC  
1321 -----+-----+-----+-----+-----+ 1380  
CCACCACCCCATGAATCTCTTTTGTAAAGGAAGAACGATACCGTTCTTGTTCCCCGTC AAG

ACTGCCCTTCTCCTCTCTGCCCCCTCCCTTGACCTTACGCCTCCAGGCTGAGGGAGGAAC  
1381 -----+-----+-----+-----+-----+ 1440  
TGACGGGAAGAGGAGAGACGGGGAAGGGAAGTGAATGCGGAGGTCCGACTCCCTCCTTG

ACTGCATCTAGACTAGGGCTCTGGTGCTGCCGAGAGTTGTTGGCAGGGCTTGGGAGAGAA  
1441 -----+-----+-----+-----+-----+ 1500  
TGACGTAGATCTGATCCCGAGACCACGACGGCTCTCAACAACCGTCCCGAACCCCTCTCTT

GAGTTCTGCAGGTGGCCTTGTTCTTCATCATCCCCCTGGTGTCATCTGTGCACCTGG  
1501 -----+-----+-----+-----+-----+ 1560  
CTCAAGACGTCCACCGGAACAAGAAGTAGTAGGGGGACACCACCGTAGACACGTGGACC

GCTGAAAAAGGCTAAAGCTGTGGAGCCTGGGTGGGTAGAAGCTTGGGTAGGTGGGACTTG  
1561 -----+-----+-----+-----+-----+ 1620  
CGACTTTTTCCCATTTTCGACACCTCGGACCCACCCATCTTCGAACCCATCCACCCTGAAC

GCTGTCACCTCCCCCTCCAACGGGGG.....  
1621 -----+-----+-----+-----+-----+ 1680

CGACAGTGGAGGGGAGGTTGCCCCC.....

.....CCAGTGAACCCAGAGACTCTTCTTTCAGGGAGGACCAGGG  
1681 -----+-----+-----+-----+ 1740  
.....GGTCACCTTGGGTCTCTGAGAAGAAAGTCCCTCCTGGTCCC

CCTTCTTTTAGAGCCATATAGTTCCTTGGGATTAGCTCTTGCCCAAGAAGGCTGAGTA  
1741 -----+-----+-----+-----+ 1800  
GGAAAGAAAATCTCGGTATATCAAGGGAACCCTAATCGAGAACGGGTTCTTCCGACTCAT

TGCCTCCCCACCTTTTAAATCCATTTTCTTTTAAATGAGGGAAATGGATATAATTT  
1801 -----+-----+-----+-----+ 1860  
ACGGAGGGGTGGAAAATTTAGGTAAAGTAAAAAAATTTACTCCCTTACCTATATTAA

TTCAGATACTAAGTAGCTGGAGAGGATGTTCTTGCTCTCCCAAAGCCCAAAGGGACAAAT  
1861 -----+-----+-----+-----+-----+ 1920  
AAGTCTATGATTTCATCGACCTCTCCTACAAGAACGAGAGGGTTTCGGGTTTCCCTGTTTA

AGGGACTTTGCTTAGGCCAAGGCAAGAGCGCAAGTGGGCACTCAGTCCTGCAGTTACCAG  
1921 -----+-----+-----+-----+-----+ 1980  
TCCCTGAAACGAATCCGGTTCCGTTCTCGCGTTCACCCGTGAGTCAGGACGTCAATGGTC

TCCTACTCCCCACTTACACTAGGGCATACTATACTATTTTACTTTTTTAAATCATAACG  
1981 -----+-----+-----+-----+-----+ 2040  
AGGATGAGGGGTGAATGTGATCCCGTATGTATATGATAAAATGAAAAATTTAGTATTGC

GCAGGAGAACAGATTTGGTTAGTTTAGAAGAAAAGGAAAACCTCTATAAATATAAATATA  
2041 -----+-----+-----+-----+-----+-----+ 2100  
CGTCCTCTTGCTAAACCAATCAAATCTCTTTTCCTTTTGGAGATATTTATATTTATAT

TATTCCTGTATTTTTATTTAATAATTTATAAATGCCAAGTTCATTGACTTTTATTTTTG  
2101 -----+-----+-----+-----+-----+-----+ 2160  
ATAAGGACATAAAAATAAATTATTAAATATTTACGGTTCAAGTAACTGAAAATAAAAC

TGTAATATGTAATGGTCGTATTAAAAATAAATAAATAAGCCCAGAAATTTAATGAGGAA  
2161 -----+-----+-----+-----+-----+-----+ 2220  
ACATTATACATTACCAGCATAATTTTTATTATTATTTCGGGTCTTTAAATTACTCCTT

AAAAAAAAAAAAAAAAACTCGAG  
2221 -----+-----+-----+-----+ 2241  
TTTTTTTTTTTTTTTGAGCTC